

1646



1646

#11

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/705,985

DATE: 07/09/2002

TIME: 16:07:59

Input Set : A:\2874-B.ST25.txt

Output Set: N:\CRF3\07092002\I705985.raw

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CENTER 1600/2900

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3 <110> APPLICANT: ANDERSON, Dirk, M.
4   GALIBERT, Laurent, J.
6 <120> TITLE OF INVENTION: METHOD OF INHIBITING OSTEOCLAST ACTIVITY
8 <130> FILE REFERENCE: 2874-B
10 <140> CURRENT APPLICATION NUMBER: 09/705,985
11 <141> CURRENT FILING DATE: 2000-11-03
13 <150> PRIOR APPLICATION NUMBER: PCT/US99/10588
14 <151> PRIOR FILING DATE: 1999-05-13
16 <150> PRIOR APPLICATION NUMBER: 60/085,487
17 <151> PRIOR FILING DATE: 1998-05-14
19 <150> PRIOR APPLICATION NUMBER: 60/110,836
20 <151> PRIOR FILING DATE: 1998-12-03
22 <150> PRIOR APPLICATION NUMBER: 08/996,139
23 <151> PRIOR FILING DATE: 1997-12-22
25 <150> PRIOR APPLICATION NUMBER: 60/064,671
26 <151> PRIOR FILING DATE: 1997-10-14
28 <150> PRIOR APPLICATION NUMBER: 60/077,181
29 <151> PRIOR FILING DATE: 1997-03-07
31 <150> PRIOR APPLICATION NUMBER: 60/059,978
32 <151> PRIOR FILING DATE: 1996-12-23
34 <160> NUMBER OF SEQ ID NOS: 8
36 <170> SOFTWARE: PatentIn version 3.1
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 3136
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (39)..(1886)
46 <223> OTHER INFORMATION:
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51                                     Met Ala Pro Arg Ala Arg
52                                     1           5
54 cgg cgc cgc ccg ctg ttc gcg ctg ctg ctg ctc tgc gcg ctg ctc gcc      104
55 Arg Arg Arg Pro Leu Phe Ala Leu Leu Leu Leu Cys Ala Leu Leu Ala
56         10           15           20
58 cgg ctg cag gtg gct ttg cag atc gct cct cca tgt acc agt gag aag      152
59 Arg Leu Gln Val Ala Leu Gln Ile Ala Pro Pro Cys Thr Ser Glu Lys
60         25           30           35
62 cat tat gag cat ctg gga cgg tgc tgt aac aaa tgt gaa cca gga aag      200
63 His Tyr Glu His Leu Gly Arg Cys Cys Asn Lys Cys Glu Pro Gly Lys
64         40           45           50

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66	tac	atg	tct	tct	aaa	tgc	act	act	acc	tct	gac	agt	gta	tgt	ctg	ccc	248
67	Tyr	Met	Ser	Ser	Lys	Cys	Thr	Thr	Thr	Ser	Asp	Ser	Val	Cys	Leu	Pro	
68	55					60					65					70	
70	tgt	ggc	ccg	gat	gaa	tac	ttg	gat	agc	tgg	aat	gaa	gaa	gat	aaa	tgc	296
71	Cys	Gly	Pro	Asp	Glu	Tyr	Leu	Asp	Ser	Trp	Asn	Glu	Glu	Asp	Lys	Cys	
72					75					80					85		
74	ttg	ctg	cat	aaa	gtt	tgt	gat	aca	ggc	aag	gcc	ctg	gtg	gcc	gtg	gtc	344
75	Leu	Leu	His	Lys	Val	Cys	Asp	Thr	Gly	Lys	Ala	Leu	Val	Ala	Val	Val	
76				90					95					100			
78	gcc	ggc	aac	agc	acg	acc	ccc	cgg	cgc	tgc	gcg	tgc	acg	gct	ggg	tac	392
79	Ala	Gly	Asn	Ser	Thr	Thr	Pro	Arg	Arg	Cys	Ala	Cys	Thr	Ala	Gly	Tyr	
80			105					110						115			
82	cac	tgg	agc	cag	gac	tgc	gag	tgc	tgc	cgc	cgc	aac	acc	gag	tgc	gcg	440
83	His	Trp	Ser	Gln	Asp	Cys	Glu	Cys	Cys	Arg	Arg	Asn	Thr	Glu	Cys	Ala	
84		120					125					130					
86	ccg	ggc	ctg	ggc	gcc	cag	cac	ccg	ttg	cag	ctc	aac	aag	gac	aca	gtg	488
87	Pro	Gly	Leu	Gly	Ala	Gln	His	Pro	Leu	Gln	Leu	Asn	Lys	Asp	Thr	Val	
88	135					140				145					150		
90	tgc	aaa	cct	tgc	ctt	gca	ggc	tac	ttc	tct	gat	gcc	ttt	tcc	tcc	acg	536
91	Cys	Lys	Pro	Cys	Leu	Ala	Gly	Tyr	Phe	Ser	Asp	Ala	Phe	Ser	Ser	Thr	
92				155					160					165			
94	gac	aaa	tgc	aga	ccc	tgg	acc	aac	tgt	acc	ttc	ctt	gga	aag	aga	gta	584
95	Asp	Lys	Cys	Arg	Pro	Trp	Thr	Asn	Cys	Thr	Phe	Leu	Gly	Lys	Arg	Val	
96			170					175					180				
98	gaa	cat	cat	ggg	aca	gag	aaa	tcc	gat	gcg	gtt	tgc	agt	tct	tct	ctg	632
99	Glu	His	His	Gly	Thr	Glu	Lys	Ser	Asp	Ala	Val	Cys	Ser	Ser	Ser	Leu	
100			185					190				195					
102	cca	gct	aga	aaa	cca	cca	aat	gaa	ccc	cat	gtt	tac	ttg	ccc	ggt	tta	680
103	Pro	Ala	Arg	Lys	Pro	Pro	Asn	Glu	Pro	His	Val	Tyr	Leu	Pro	Gly	Leu	
104		200					205					210					
106	ata	att	ctg	ctt	ctc	ttc	gcg	tct	gtg	gcc	ctg	gtg	gct	gcc	atc	atc	728
107	Ile	Ile	Leu	Leu	Leu	Phe	Ala	Ser	Val	Ala	Leu	Val	Ala	Ala	Ile	Ile	
108	215					220				225					230		
110	ttt	ggc	gtt	tgc	tat	agg	aaa	aaa	ggg	aaa	gca	ctc	aca	gct	aat	ttg	776
111	Phe	Gly	Val	Cys	Tyr	Arg	Lys	Lys	Gly	Lys	Ala	Leu	Thr	Ala	Asn	Leu	
112				235					240					245			
114	tgg	cac	tgg	atc	aat	gag	gct	tgt	ggc	cgc	cta	agt	gga	gat	aag	gag	824
115	Trp	His	Trp	Ile	Asn	Glu	Ala	Cys	Gly	Arg	Leu	Ser	Gly	Asp	Lys	Glu	
116			250					255					260				
118	tcc	tca	ggt	gac	agt	tgt	gtc	agt	aca	cac	acg	gca	aac	ttt	ggt	cag	872
119	Ser	Ser	Gly	Asp	Ser	Cys	Val	Ser	Thr	His	Thr	Ala	Asn	Phe	Gly	Gln	
120			265					270					275				
122	cag	gga	gca	tgt	gaa	ggt	gtc	tta	ctg	ctg	act	ctg	gag	gag	aag	aca	920
123	Gln	Gly	Ala	Cys	Glu	Gly	Val	Leu	Leu	Leu	Thr	Leu	Glu	Glu	Lys	Thr	
124		280					285					290					
126	ttt	cca	gaa	gat	atg	tgc	tac	cca	gat	caa	ggt	ggt	gtc	tgt	cag	ggc	968
127	Phe	Pro	Glu	Asp	Met	Cys	Tyr	Pro	Asp	Gln	Gly	Gly	Val	Cys	Gln	Gly	
128	295					300				305					310		
130	acg	tgt	gta	gga	ggt	ggt	ccc	tac	gca	caa	ggc	gaa	gat	gcc	agg	atg	1016

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131	Thr	Cys	Val	Gly	Gly	Gly	Pro	Tyr	Ala	Gln	Gly	Glu	Asp	Ala	Arg	Met	
132				315						320					325		
134	ctc	tca	ttg	gtc	agc	aag	acc	gag	ata	gag	gaa	gac	agc	ttc	aga	cag	1064
135	Leu	Ser	Leu	Val	Ser	Lys	Thr	Glu	Ile	Glu	Glu	Asp	Ser	Phe	Arg	Gln	
136				330					335					340			
138	atg	ccc	aca	gaa	gat	gaa	tac	atg	gac	agg	ccc	tcc	cag	ccc	aca	gac	1112
139	Met	Pro	Thr	Glu	Asp	Glu	Tyr	Met	Asp	Arg	Pro	Ser	Gln	Pro	Thr	Asp	
140			345					350					355				
142	cag	tta	ctg	ttc	ctc	act	gag	cct	gga	agc	aaa	tcc	aca	cct	cct	ttc	1160
143	Gln	Leu	Leu	Phe	Leu	Thr	Glu	Pro	Gly	Ser	Lys	Ser	Thr	Pro	Pro	Phe	
144		360					365					370					
146	tct	gaa	ccc	ctg	gag	gtg	ggg	gag	aat	gac	agt	tta	agc	cag	tgc	ttc	1208
147	Ser	Glu	Pro	Leu	Glu	Val	Gly	Glu	Asn	Asp	Ser	Leu	Ser	Gln	Cys	Phe	
148	375					380				385						390	
150	acg	ggg	aca	cag	agc	aca	gtg	ggg	tca	gaa	agc	tgc	aac	tgc	act	gag	1256
151	Thr	Gly	Thr	Gln	Ser	Thr	Val	Gly	Ser	Glu	Ser	Cys	Asn	Cys	Thr	Glu	
152				395					400					405			
154	ccc	ctg	tgc	agg	act	gat	tgg	act	ccc	atg	tcc	tct	gaa	aac	tac	ttg	1304
155	Pro	Leu	Cys	Arg	Thr	Asp	Trp	Thr	Pro	Met	Ser	Ser	Glu	Asn	Tyr	Leu	
156			410						415					420			
158	caa	aaa	gag	gtg	gac	agt	ggc	cat	tgc	ccg	cac	tgg	gca	gcc	agc	ccc	1352
159	Gln	Lys	Glu	Val	Asp	Ser	Gly	His	Cys	Pro	His	Trp	Ala	Ala	Ser	Pro	
160		425					430						435				
162	agc	ccc	aac	tgg	gca	gat	gtc	tgc	aca	ggc	tgc	cgg	aac	cct	cct	ggg	1400
163	Ser	Pro	Asn	Trp	Ala	Asp	Val	Cys	Thr	Gly	Cys	Arg	Asn	Pro	Pro	Gly	
164		440				445						450					
166	gag	gac	tgt	gaa	ccc	ctc	gtg	ggg	tcc	cca	aaa	cgt	gga	ccc	ttg	ccc	1448
167	Glu	Asp	Cys	Glu	Pro	Leu	Val	Gly	Ser	Pro	Lys	Arg	Gly	Pro	Leu	Pro	
168	455					460				465						470	
170	cag	tgc	gcc	tat	ggc	atg	ggc	ctt	ccc	cct	gaa	gaa	gaa	gcc	agc	agg	1496
171	Gln	Cys	Ala	Tyr	Gly	Met	Gly	Leu	Pro	Pro	Glu	Glu	Glu	Ala	Ser	Arg	
172				475					480						485		
174	acg	gag	gcc	aga	gac	cag	ccc	gag	gat	ggg	gct	gat	ggg	agg	ctc	cca	1544
175	Thr	Glu	Ala	Arg	Asp	Gln	Pro	Glu	Asp	Gly	Ala	Asp	Gly	Arg	Leu	Pro	
176			490						495					500			
178	agc	tca	gcg	agg	gca	ggg	gcc	ggg	tct	gga	agc	tcc	cct	ggg	ggc	cag	1592
179	Ser	Ser	Ala	Arg	Ala	Gly	Ala	Gly	Ser	Gly	Ser	Ser	Pro	Gly	Gly	Gln	
180			505					510						515			
182	tcc	cct	gca	tct	gga	aat	gtg	act	gga	aac	agt	aac	tcc	acg	ttc	atc	1640
183	Ser	Pro	Ala	Ser	Gly	Asn	Val	Thr	Gly	Asn	Ser	Asn	Ser	Thr	Phe	Ile	
184		520				525						530					
186	tcc	agc	ggg	cag	gtg	atg	aac	ttc	aag	ggc	gac	atc	atc	gtg	gtc	tac	1688
187	Ser	Ser	Gly	Gln	Val	Met	Asn	Phe	Lys	Gly	Asp	Ile	Ile	Val	Val	Tyr	
188	535					540					545					550	
190	gtc	agc	cag	acc	tcg	cag	gag	ggc	gcg	gcg	gcg	gct	gcg	gag	ccc	atg	1736
191	Val	Ser	Gln	Thr	Ser	Gln	Glu	Gly	Ala	Ala	Ala	Ala	Ala	Glu	Pro	Met	
192				555						560					565		
194	ggc	cgc	ccg	gtg	cag	gag	gag	acc	ctg	gcg	cgc	cga	gac	tcc	ttc	gcg	1784
195	Gly	Arg	Pro	Val	Gln	Glu	Glu	Thr	Leu	Ala	Arg	Arg	Asp	Ser	Phe	Ala	

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196          570          575          580
198 ggg aac ggc ccg cgc ttc ccg gac ccg tgc ggc ggc ccc gag ggg ctg      1832
199 Gly Asn Gly Pro Arg Phe Pro Asp Pro Cys Gly Gly Pro Glu Gly Leu
200          585          590          595
202 cgg gag ccg gag aag gcc tgc agg ccg gtg cag gag caa ggc ggg gcc      1880
203 Arg Glu Pro Glu Lys Ala Ser Arg Pro Val Gln Glu Gln Gly Gly Ala
204          600          605          610
206 aag gct tgagcgcccc ccatggctgg gagcccgaag ctcgagacca gggctcgca      1936
207 Lys Ala
208 615
210 gggcagcacc gcagcctctg cccagcccc ggccaccag ggatcgatcg gtacagtcga      1996
212 ggaagaccac ccggcattct ctgccactt tgccttcag gaaatgggct tttcaggaag      2056
214 tgaattgatg aggactgtcc ccatgccac ggatgctcag cagcccgccg cactggggca      2116
216 gatgtctccc ctgccactcc tcaaactcgc agcagtaatt tgtggcaacta tgacagctat      2176
218 ttttatgact atcctgttct gtgggggggg ggtctatgtt tccccccat atttgtattc      2236
220 cttttcataa cttttcttga tatctttcct ccctcttttt taatgtaaag gttttctcaa      2296
222 aaattctcct aaagggtgagg gtctctttct tttctctttt cttttttttt ttcttttttt      2356
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236 aaacactttt gggaaagggc taaacatgtg aggcctggag atagttgcta agttgctagg      2776
238 aacatgtggt gggactttca tattctgaaa aatgttctat attctcattt ttctaaaaga      2836
240 aagaaaaaag gaaacccgat ttatttctcc tgaatctttt taagtttggt tcgttcctta      2896
242 agcagaacta agctcagtat gtgaccttac ccgctaggtg gttaatttat ccatgctggc      2956
244 agaggcactc aggtacttgg taagcaaatt tctaaaactc caagttgctg cagcttggca      3016
246 ttcttcttat tctagaggtc tctctggaaa agatggagaa aatgaacagg acatggggct      3076
248 cctggaaaga aagggcccg gaagttcaag gaagaataaa gttgaaattt taaaaaaaaa      3136
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253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 2
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263          20          25          30
266 Pro Cys Thr Ser Glu Lys His Tyr Glu His Leu Gly Arg Cys Cys Asn
267          35          40          45
270 Lys Cys Glu Pro Gly Lys Tyr Met Ser Ser Lys Cys Thr Thr Thr Ser
271          50          55          60
274 Asp Ser Val Cys Leu Pro Cys Gly Pro Asp Glu Tyr Leu Asp Ser Trp
275 65          70          75          80
278 Asn Glu Glu Asp Lys Cys Leu Leu His Lys Val Cys Asp Thr Gly Lys
279          85          90          95
282 Ala Leu Val Ala Val Val Ala Gly Asn Ser Thr Thr Pro Arg Arg Cys
283          100          105          110

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286 Ala Cys Thr Ala Gly Tyr His Trp Ser Gln Asp Cys Glu Cys Cys Arg
287      115      120      125
290 Arg Asn Thr Glu Cys Ala Pro Gly Leu Gly Ala Gln His Pro Leu Gln
291      130      135      140
294 Leu Asn Lys Asp Thr Val Cys Lys Pro Cys Leu Ala Gly Tyr Phe Ser
295 145      150      155      160
298 Asp Ala Phe Ser Ser Thr Asp Lys Cys Arg Pro Trp Thr Asn Cys Thr
299      165      170      175
302 Phe Leu Gly Lys Arg Val Glu His His Gly Thr Glu Lys Ser Asp Ala
303      180      185      190
306 Val Cys Ser Ser Ser Leu Pro Ala Arg Lys Pro Pro Asn Glu Pro His
307      195      200      205
310 Val Tyr Leu Pro Gly Leu Ile Ile Leu Leu Leu Phe Ala Ser Val Ala
311      210      215      220
314 Leu Val Ala Ala Ile Ile Phe Gly Val Cys Tyr Arg Lys Lys Gly Lys
315 225      230      235      240
318 Ala Leu Thr Ala Asn Leu Trp His Trp Ile Asn Glu Ala Cys Gly Arg
319      245      250      255
322 Leu Ser Gly Asp Lys Glu Ser Ser Gly Asp Ser Cys Val Ser Thr His
323      260      265      270
326 Thr Ala Asn Phe Gly Gln Gln Gly Ala Cys Glu Gly Val Leu Leu Leu
327      275      280      285
330 Thr Leu Glu Glu Lys Thr Phe Pro Glu Asp Met Cys Tyr Pro Asp Gln
331      290      295      300
334 Gly Gly Val Cys Gln Gly Thr Cys Val Gly Gly Gly Pro Tyr Ala Gln
335 305      310      315      320
338 Gly Glu Asp Ala Arg Met Leu Ser Leu Val Ser Lys Thr Glu Ile Glu
339      325      330      335
342 Glu Asp Ser Phe Arg Gln Met Pro Thr Glu Asp Glu Tyr Met Asp Arg
343      340      345      350
346 Pro Ser Gln Pro Thr Asp Gln Leu Leu Phe Leu Thr Glu Pro Gly Ser
347      355      360      365
350 Lys Ser Thr Pro Pro Phe Ser Glu Pro Leu Glu Val Gly Glu Asn Asp
351      370      375      380
354 Ser Leu Ser Gln Cys Phe Thr Gly Thr Gln Ser Thr Val Gly Ser Glu
355 385      390      395      400
358 Ser Cys Asn Cys Thr Glu Pro Leu Cys Arg Thr Asp Trp Thr Pro Met
359      405      410      415
362 Ser Ser Glu Asn Tyr Leu Gln Lys Glu Val Asp Ser Gly His Cys Pro
363      420      425      430
366 His Trp Ala Ala Ser Pro Ser Pro Asn Trp Ala Asp Val Cys Thr Gly
367      435      440      445
370 Cys Arg Asn Pro Pro Gly Glu Asp Cys Glu Pro Leu Val Gly Ser Pro
371      450      455      460
374 Lys Arg Gly Pro Leu Pro Gln Cys Ala Tyr Gly Met Gly Leu Pro Pro
375 465      470      475      480
378 Glu Glu Glu Ala Ser Arg Thr Glu Ala Arg Asp Gln Pro Glu Asp Gly
379      485      490      495
382 Ala Asp Gly Arg Leu Pro Ser Ser Ala Arg Ala Gly Ala Gly Ser Gly

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VERIFICATION SUMMARY

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